

Sandals, W.

1636

#7

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/378,528B

DATE: 03/29/2000  
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Input Set: I378528B.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

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JC 1600 MAIL ROOM

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1 <110> APPLICANT: Nabel, Elizabeth G.
2 Nabel, Gary J.
3 <120> TITLE OF INVENTION: Inhibition of Smooth Muscle Cell Migration by Heme
4 Oxygenase I
5 <130> FILE REFERENCE: 8642/72
6 <140> CURRENT APPLICATION NUMBER: US/09/378,528B
7 <141> CURRENT FILING DATE: 1999-08-20
8 <150> EARLIER APPLICATION NUMBER: 60/097,707
9 <151> EARLIER FILING DATE: 1998-08-21
10 <160> NUMBER OF SEQ ID NOS: 4
11 <170> SOFTWARE: PatentIn Ver. 2.0
12 <210> SEQ ID NO 1
13 <211> LENGTH: 1550
14 <212> TYPE: DNA
15 <213> ORGANISM: Homo sapiens
16 <400> SEQUENCE: 1
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18 acgagcccag caccggccgg atggagcgtc cgcaaccga cagcatgccc caggatttgt 120
19 cagaggccct gaaggaggcc accaaggagg tgcacacca ggcagagaat gctgagttca 180
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22 tcgccccctg ctacttccca gaagagctgc accgcaaggc tgccctggag caggacctgg 360
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29 ttgaggagtt gcaggagctg ctgacctatg acaccaagga ccagagcccc tcacgggcac 780
30 cagggcttcg ccagcggggc agcaacaaag tgcaagattc tgccccctg gagactccca 840
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43 <210> SEQ ID NO 2
44 <211> LENGTH: 288
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PAGE: 2

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/378,528B

DATE: 03/29/2000  
TIME: 15:36:09

Input Set: I378528B.RAW

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51      20          25          30
52 Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr Arg Asp Gly Phe Lys
53      35          40          45
54 Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu
55      50          55          60
56 Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro
57      65          70          75          80
58 Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln Asp Leu Ala Phe Trp
59      85          90          95
60 Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr Thr Pro Ala Met Gln
61      100         105         110
62 Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg Thr Glu Pro Glu Leu
63      115         120         125
64 Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly Asp Leu Ser Gly Gly
65      130         135         140
66 Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu Asp Leu Pro Ser Ser
67      145         150         155
68 Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn Ile Ala Ser Ala Thr
69      165         170         175
70 Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn Ser Leu Glu Met Thr
71      180         185         190
72 Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala Lys Thr Ala Phe Leu
73      195         200         205
74 Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu Leu Leu Thr His Asp
75      210         215         220
76 Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly Leu Arg Gln Arg Ala
77      225         230         235         240
78 Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu Thr Pro Arg Gly Lys
79      245         250         255
80 Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu Leu Arg Trp Val Leu
81      260         265         270
82 Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val Gly Leu Tyr Ala Met
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88 <220> FEATURE:
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93 <211> LENGTH: 19
94 <212> TYPE: DNA

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PAGE: 3

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98 <400> SEQUENCE: 4  
99 gtgcccacgg taaggaagc

19

PAGE: 4

VERIFICATION SUMMARY  
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